```
=> fil reg; d que l2
FILE 'REGISTRY' ENTERED AT 10:55:23 ON 12 AUG 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES:   11 AUG 2003  HIGHEST RN 565156-77-6
DICTIONARY FILE UPDATES:  11 AUG 2003  HIGHEST RN 565156-77-6

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Crossover limits have been increased.  See HELP CROSSOVER for details.

Experimental and calculated property data are now available.  See HELP
PROPERTIES for more information.  See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf


L2            22 SEA FILE=REGISTRY ABB=ON  E[QSHYE][SQITNP][FTSPLI][NSKMTD][DKTE
                 ][FLRI][TSN]R[IVA]/SQSP      R8    R7    R6    R5    R4
                   R3   R2   R1

=> d rn cn sql kwic nte lc l2 1-22

L2   ANSWER 1 OF 22  REGISTRY  COPYRIGHT 2003 ACS on STN
RN   549605-92-7  REGISTRY - Use Registry # to match seq. to citation
CN   2217: PN: WO03008540 SEQID: 8061 unclaimed protein (9CI)  (CA INDEX NAME)
SQL  430
SQL = sequence length
SEQ    351 QQQKVAFLFC CGCSMCEETL TDRNRVKKAQ QYHLPTPNRI SGLETSHRRT
                      ==== ======

HITS AT:   367-376
LC   STN Files:   CA, CAPLUS, TOXCENTER

L2   ANSWER 2 OF 22  REGISTRY  COPYRIGHT 2003 ACS on STN
RN   524076-00-4  REGISTRY
CN   10: PN: US6566583 SEQID: 10 unclaimed protein (9CI)  (CA INDEX NAME)
SQL  543

SEQ      1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF
                                  = =========

HITS AT:   30-39

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, USPATFULL

L2   ANSWER 3 OF 22  REGISTRY  COPYRIGHT 2003 ACS on STN
RN   500231-10-7  REGISTRY
CN   1: PN: WO03015517 SEQID: 1 claimed protein (9CI)  (CA INDEX NAME)
SQL  635

SEQ    551 LTEFETRFRR ILKRVYRSLQ QHEIREEILD ERSRIQWQWQ QLASVVDRLL
                      ===== =====

HITS AT:   576-585

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
```

LC STN Files: CA, CAPLUS

L2 ANSWER 4 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 489862-35-3 REGISTRY
CN GenBank CAA58438 (9CI) (CA INDEX NAME) — GenBank records printed at end of search (no citations in bibliographic dbs)
OTHER NAMES:
CN GenBank CAA58438 (Translated from: GenBank X83413)
SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV
= =========
HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 5 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 485151-28-8 REGISTRY
CN GenBank AAA81080 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAA81080 (Translated from: GenBank U39855)
SQL 672

SEQ 601 SASSNSVLTE FETRFRRILK RVYRSLQQHE IREEILDERS RIQCSGNNLH
======== ==
HITS AT: 633-642

L2 ANSWER 6 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 485104-00-5 REGISTRY
CN GenBank AAA46012 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAA46012 (Translated from: GenBank M87287)
SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV
= =========
HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 7 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 483502-77-8 REGISTRY
CN GenBank BAB17787 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAB17787 (Translated from: GenBank AB042530)
SQL 1851

SEQ 101 YFPGLCNYVF SEHCGAAYED FNIQLRRGLE SNSTTLSRVI MKLDGLVVEL
= =========
HITS AT: 130-139
NTE

type	------ location ------	description
uncommon	Aaa-1846 -	-

L2 ANSWER 8 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 459531-51-2 REGISTRY
CN GenBank AAB81126 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB81126 (Translated from: GenBank U73935)
SQL 543

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF
= =========

HITS AT: 30-39

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 9 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 406671-25-8 REGISTRY
CN Prefoldin, molecular chaperone implicated in de novo protein folding (Methanopyrus kandleri strain AV19 gene GIM5) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAM02827
CN GenBank AAM02827 (Translated from: GenBank AE010451)
SQL 157

SEQ 1 MAEKKNEQEI QQELQRLIAE INRLQGQMEA INAQIDLIES SISELNRVEE
== ========

HITS AT: 39-48
LC STN Files: CA, CAPLUS - this RN does have citation in CAPLUS

L2 ANSWER 10 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 356608-55-4 REGISTRY
CN 5-HT3 receptor (Caenorhabditis elegans clone F18G5.4 635-amino acid isoform) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 10: PN: WO0161000 SEQID: 10 claimed protein
SQL 635

SEQ 551 LTEFETRFRR ILKRVYRSLQ QHEIREEILD ERSRIQWQWQ QLASVVDRLL
===== =====

HITS AT: 576-585

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 11 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 353881-58-0 REGISTRY
CN Galactose-1-phosphate uridyltransferase (Clostridium acetobutylicum strain ATCC 824 gene CAC2961) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK80903
CN GenBank AAK80903 (Translated from: GenBank AE007793)
SQL 497

SEQ 201 LNKSKWFLQY SPYTYYNEHC IILNNEHIPM KISRITFENL LSFIDILPHY
===== =====

HITS AT: 226-235
LC STN Files: CA, CAPLUS

L2 ANSWER 12 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 348670-68-8 REGISTRY
CN Protein (Sulfolobus solfataricus gene SSO2259) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK42425
CN GenBank AAK42425 (Translated from: GenBank AE006830)
SQL 220

SEQ 101 KGILDPIIGL LEDEESLGKI INALINDFTL NLINHWEEII NDLSRIDLTN
==== ======

HITS AT: 137-146
LC STN Files: CA, CAPLUS

L2 ANSWER 13 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN

RN 342056-52-4 REGISTRY
CN Protein (Shewanella putrefaciens 542-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: JP2001145490 SEQID: 13 claimed protein
SQL 542

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF
= =========
HITS AT: 30-39
LC STN Files: CA, CAPLUS

L2 ANSWER 14 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 325762-37-6 REGISTRY
CN Blood-coagulation factor X, prepro-[227-serine,228-glutamine,229-threonine,230-serine,231-lysine,232-leucine,233-threonine] (human liver) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 8: PN: WO0110896 SEQID: 2 claimed protein
SQL 488

SEQ 201 KPYDAADLDP TENPFDLLDF NQTQPESQTS KLTRIVGGQE CKDGECPWQA
===== =====
HITS AT: 226-235
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 15 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 325762-36-5 REGISTRY
CN Blood-coagulation factor X, prepro-[227-glutamine,228-serine,229-phenylalanine,230-asparagine,231-aspartic acid,232-phenylalanine,233-threonine] (human liver) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: WO0110896 SEQID: 2 claimed protein
SQL 488

SEQ 201 KPYDAADLDP TENPFDLLDF NQTQPEQSFN DFTRIVGGQE CKDGECPWQA
===== =====
HITS AT: 226-235
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 16 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 303239-87-4 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173674) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1354: PN: EP1033405 SEQID: 66354 claimed protein
SQL 151

SEQ 1 MPCSSDHEAW MKCYKENIGS PLKCSGFVKS FQDCARRSRQ QVNPEENSNT
======
51 LNRVNLGEQI FLSIFNVMTR MMLGAIVEEE ERTILGNELK KLILLFQISK
====
HITS AT: 45-54
LC STN Files: CA, CAPLUS

L2 ANSWER 17 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 303239-86-3 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173673) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1353: PN: EP1033405 SEQID: 66353 claimed protein
SQL 217

SEQ 101 ARRSRQQVNP EENSNTLNRV NLGEQIFLSI FNVMTRMMLG AIVEEEERTI
==========
HITS AT: 111-120

LC STN Files: CA, CAPLUS

L2 ANSWER 18 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 303239-85-2 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173672) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1352: PN: EP1033405 SEQID: 66352 claimed protein
SQL 274

SEQ 151 VKSFQDCARR SRQQVNPEEN SNTLNRVNLG EQIFLSIFNV MTRMMLGAIV
=== =======

HITS AT: 168-177
LC STN Files: CA, CAPLUS

L2 ANSWER 19 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 167975-38-4 REGISTRY
CN Phosphoprotein (human herpesvirus 6 strain U1102 gene U11) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Phosphoprotein (human herpes virus 6 strain U1102 gene U11)
SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV
= =========

HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 20 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 153926-89-7 REGISTRY
CN Protein (Shewanella putrefaciens clone pEPA 543-amino acid reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein (Shewanella putrefaciens strain SCRC-2874 open reading frame ORF9)
CN Protein (Shewanella tumefaciens clone pEPA open reading frame ORF9)
SQL 543

MGRP

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF
= =========

HITS AT: 30-39

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 21 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 153676-37-0 REGISTRY
CN Protein (human herpesvirus 6 strain U1102 gene P1LF1) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein (human herpes virus 6 strain U1102 gene P1LF1)
OTHER NAMES:
CN GenBank AAA16716
CN GenBank AAA16716 (Translated from: GenBank L25528)
SQL 871

SEQ 101 NSKGLNKGIF ENMFTNKEKF ESQFSDINRA LLRLGNFIKW GSNVAIDTPY
==========

HITS AT: 121-130
LC STN Files: CA, CAPLUS

L2 ANSWER 22 OF 22 REGISTRY COPYRIGHT 2003 ACS on STN
RN 147156-14-7 REGISTRY

Searched by Barb O'Bryen, STIC 308-4291

CN Protein p 100 (human herpesvirus 6 clone pDF446-4/pDF446-3/pD2Hae/pMF101R) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein p 100 (human herpes virus 6 clone pDF446-4/pDF446-3/pD2Hae/pMF101R)
OTHER NAMES:
CN P100 capsid protein (human herpesvirus 6)
SQL 869

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV
= =========
HITS AT: 120-129
LC STN Files: CA, CAPLUS, MEDLINE, TOXCENTER, USPATFULL

=> fil capl uspatf medl toxcenter; s l2
FILE 'CAPLUS' ENTERED AT 10:56:31 ON 12 AUG 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 10:56:31 ON 12 AUG 2003
CA INDEXING COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MEDLINE' ENTERED AT 10:56:31 ON 12 AUG 2003

FILE 'TOXCENTER' ENTERED AT 10:56:31 ON 12 AUG 2003
COPYRIGHT (C) 2003 ACS

L3 34 L2 Registry answer set crossed into bibliographic files to get citations

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 26 DUP REM L3 (8 DUPLICATES REMOVED)
ANSWERS '1-21' FROM FILE CAPLUS
ANSWERS '22-24' FROM FILE USPATFULL
ANSWERS '25-26' FROM FILE MEDLINE

=> d ibib ab hitrn 1-24; d iall 25-26; fil hom

L4 ANSWER 1 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2003:539800 CAPLUS
DOCUMENT NUMBER: 139:64475
TITLE: Abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant
INVENTOR(S): Kreps, Joel; Briggs, Steven P.; Cooper, Bret; Glazebrook, Jane; Goff, Stephen A.; Katagiri, Fumiyaki; Moughamer, Todd; Provart, Nicholas; Ricke, Darrell; Zhu, Tong
PATENT ASSIGNEE(S): Syngenta Participations AG, Switz.
SOURCE: PCT Int. Appl., 177 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 8
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008540	A2	20030130	WO 2002-XA19668	20020621

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2003008540 A2 20030130 WO 2002-US19668 20020621
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003135888 A1 20030717 US 2002-259165 20020926
PRIORITY APPLN. INFO.: US 2001-300112P P 20010622
US 2001-314662P P 20010824
US 2001-325277P P 20010926
US 2001-332132P P 20011121
WO 2002-US19668 A 20020621
US 2002-368327P P 20020327
US 2002-370620P P 20020404

AB Abiotic stress responsive polynucleotides and polypeptides are disclosed. Also disclosed are vectors, expression cassettes, host cells, and plants contg. such polynucleotides. Also provided are methods for using such polynucleotides and polypeptides, for example, to alter the responsiveness of a plant to abiotic stress. Rice (Oryza sativa japonica) cDNA library was constructed and sequenced, and used in GeneChip std. protocol for expression profiling of stress-regulated genes. Based on the profiles, clusters of nucleic sequences that were altered at least two-fold in response to the stress condition were identified. Identification of abiotic stress responsive genes using yeast two hybrid system was also demonstrated. Rice orthologs of Arabidopsis abiotic stress genes were identified by reverse genetics. Transgenic rice expressing "abiotic stress candidate gene" was produced. The present invention claimed abiotic stress responsive cDNAs (SEQ IDs 1-4131, 8263-8353, 8445-8829 and 17505-17506) and proteins (SEQ IDs 4132-8262, 8354-8444, and 8830-9214), but the Sequence Listing was not made available on publication of the patent application.

IT **549605-92-7** Use Registry # to match citation to sequence
RL: PRP (Properties)
(unclaimed protein sequence; abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant)

L4 ANSWER 2 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2003:390870 CAPLUS
DOCUMENT NUMBER: 138:380503
TITLE: Protein and cDNA sequences of a Schizochytrium aggregatum polyketide-like synthase (PKS-like) gene and use
INVENTOR(S): Facciotti, Daniel; Metz, James George; Lassner, Michael
PATENT ASSIGNEE(S): USA
SOURCE: U.S., 261 pp., Cont.-in-part of U.S. 6,140,486.
CODEN: USXXAM
DOCUMENT TYPE: Patent

Searched by Barb O'Bryen, STIC 308-4291

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6566583	B1	20030520	US 1999-231899	19990114
US 6140486	A	20001031	US 1998-90793	19980604
CA 2359629	AA	20000720	CA 2000-2359629	20000114
WO 2000042195	A2	20000720	WO 2000-US956	20000114
WO 2000042195	A3	20000928		

W: BR, CA, IL, JP, MX
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

EP 1147197	A2	20011024	EP 2000-904357	20000114

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

BR 2000008760	A	20021008	BR 2000-8760	20000114
JP 2002534123	T2	20021015	JP 2000-593752	20000114
US 2002194641	A1	20021219	US 2002-124800	20020416
US 2003101486	A1	20030529	US 2002-331061	20021227

PRIORITY APPLN. INFO.:

US 1997-48650P	P	19970604
US 1998-90793	A2	19980604
US 1999-231899	A	19990114
WO 2000-US956	W	20000114
US 2001-284066P	P	20010416
US 2001-298796P	P	20010615
US 2001-323269P	P	20010918

AB The present invention provides protein and cDNA sequences of a novel Schizochytrium aggregatum polyketide-like synthesis (PKS-like) gene. The present invention relates to compns. and methods for prepg. poly-unsatd. long chain fatty acids in plants, plant parts and plant cells, such as leaves, roots, fruits and seeds. Nucleic acid sequences and constructs encoding PKS-like genes required for the poly-unsatd. long chain fatty acid prodn., including the genes responsible for eicosapentenoic acid prodn. of Shewanella putrefaciens and novel genes assocd. with the prodn. of docosahexaenoic acid in Vibrio marinus are used to generate transgenic plants, plant parts and cells which contain and express one or more transgenes encoding one or more of the PKS-like genes assocd. with such long chain polyunsatd. fatty acid prodn. Expression of the PKS-like genes in the plant system permits the large scale prodn. of poly-unsatd. long chain fatty acids such as eicosapentenoic acid and docosahexaenoic acid for modification of the fatty acid profile of plants, plant parts and tissues. Manipulation of the fatty acid profiles allows for the prodn. of com. quantities of novel plant oils and products.

IT **524076-00-4**
RL: PRP (Properties)
(unclaimed protein sequence; protein and cDNA sequences of a Schizochytrium aggregatum polyketide-like synthase (PKS-like) gene and use)

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2001:115178 CAPLUS
DOCUMENT NUMBER: 134:168320
TITLE: Factor X substitution mutant with an improved ability to be activated
INVENTOR(S): Himmelspach, Michele; Schlokat, Uwe
PATENT ASSIGNEE(S): Baxter A.-G., Austria
SOURCE: PCT Int. Appl., 50 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

Searched by Barb O'Bryen, STIC 308-4291

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001010896	A2	20010215	WO 2000-EP7631	20000807
WO 2001010896	A3	20020711		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AT 9901377	A	20020715	AT 1999-1377	19990810
AT 410216	B	20030325		
EP 1238065	A2	20020911	EP 2000-949465	20000807

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL

PRIORITY APPLN. INFO.: AT 1999-1377 A 19990810
WO 2000-EP7631 W 20000807

OTHER SOURCE(S): MARPAT 134:168320

AB The invention relates to factor Xa analogs with a modified protease cleavage site, comprising a substitution of a min. of one of the amino acid between Glu226 and Arg234 and possibly Ile235 in the region of activation peptide. These modified cleavage sites in the region of activation peptide change protease specificity and facilitate factor XIa cleavage of the precursor. The invention also relates to prepns. contg. said factor Xa analogs and methods for the prodn. thereof. The prepro-factor X analogs may be used to produce high-purity factor X for use as coagulants.

IT **325762-36-5P 325762-37-6P**
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; factor X substitution mutant with improved ability to be activated)

L4 ANSWER 4 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 1998:572263 CAPLUS
DOCUMENT NUMBER: 129:212504
TITLE: Genes coding for eicosapentaenoic acid synthetic enzymes and use for production of eicosapentaenoic acid in Escherichia coli
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: U.S., 81 pp., Cont.-in-part of U.S. 5,683,898.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5798259	A	19980825	US 1996-752929	19961120
US 5683898	A	19971104	US 1995-375709	19950120

PRIORITY APPLN. INFO.: JP 1992-147945 19920515

US 1994-178251 19940110
US 1995-375709 19950120

AB Claimed are DNA sequences encoding eicosapentaenoic acid (EPA) biosynthetic enzymes derived from Shewanella putrefaciens, and their cloning in Escherichia coli for the prodn. of EPA. There is provided an advantageous process for prodn. of EPA by a recombinant technique wherein genes coding for EPA biosynthesis enzymes useful as pharmaceuticals, agrochems., foods, feeds or the like are obtained from microorganisms. EPA is produced by obtaining genes coding for eicosapentaenoic acid (EPA) biosynthesis enzymes, constructing a plasmid by joining the genes to a vector, transforming E. coli with the plasmid, and culturing the transformed E. coli.

IT **153926-89-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes coding for eicosapentaenoic acid synthetic enzymes and use for prodn. of eicosapentaenoic acid in E. coli)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 1997:719630 CAPLUS
DOCUMENT NUMBER: 128:10898
TITLE: Sequence of Shewanella putrefaciens gene coding for 9 eicosapentaenoic acid synthesizing enzymes and process for production of eicosapentaenoic acid with expression in Escherichia coli using pEPA vector
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: U.S., 77 pp., Cont.-in-part of U.S. Ser. No. 178,251, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5683898	A	19971104	US 1995-375709	19950120
US 5798259	A	19980825	US 1996-752929	19961120
PRIORITY APPLN. INFO.:			JP 1992-147945	19920515
			US 1994-178251	19940110
			US 1995-375709	19950120

AB There is provided an advantageous process for prodn. of EPA by a gene recombinant technique wherein genes coding for biosynthesis enzymes for eicosapentaenoic acid (EPA) useful as pharmaceuticals, agrochems., foods, feeds or the like is obtained from microorganisms. EPA is produced by obtaining genes coding for eicosapentaenoic acid (EPA) biosynthesis enzymes, constructing a plasmid by joining the genes to a vector, transforming E. coli with the plasmid, and culturing the transformed E. coli.

IT **153926-89-7P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; Shewanella putrefaciens genes encoding eicosapentaenoic acid synthesizing enzymes and prodn. of eicosapentaenoic acid with Escherichia coli)

L4 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 1993:210909 CAPLUS
DOCUMENT NUMBER: 118:210909

TITLE: Gene for the major antigenic structural protein (p100) of human herpesvirus 6
AUTHOR(S): Neipel, Frank; Ellinger, Klaus; Fleckenstein, Bernhard
CORPORATE SOURCE: Inst. Klin. Mol. Virol., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Journal of Virology (1992), 66(6), 3918-24
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A human herpesvirus 6 (HHV-6) structural protein of 100 kDa (p100) is the polypeptide most frequently and intensively reactive in immunoblotting analyses with human sera on HHV-6-infected cells or partially purified virions. The gene for p100 was identified by screening a bacteriophage lambda library with monospecific rabbit antisera. The gene codes for a polypeptide of 870 amino acids with a calcd. mol. size of 97 kDa. Its N-terminal third is weakly homologous to the immunogenic basic matrix phosphoprotein pp150 of human cytomegalovirus. Five fragments representing more than 93% of HHV-6 p100 were prokaryotically expressed. The antigenic epitopes of p100 were preliminarily mapped by immunoblotting with human sera. They are located within the C-terminal part which is neither homologous nor cross-reactive to pp150 of human cytomegalovirus. Availability of the gene for the immunodominant structural protein should provide tools for studies of pathogenesis by HHV-6.

IT **147156-14-7**
RL: PRP (Properties)
(amino acid sequence of, complete)

L4 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2003:154153 CAPLUS
DOCUMENT NUMBER: 138:200330
TITLE: Agonists and antagonists of 5-HT3-like receptors of invertebrates as pesticides
INVENTOR(S): Trowell, Stephen Charles; Saubern, Simon; Liao, Chunyan
PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organisation, Australia
SOURCE: PCT Int. Appl., 53 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003015517	A1	20030227	WO 2002-AU1096	20020814

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: AU 2001-7011 A 20010814
OTHER SOURCE(S): MARPAT 138:200330

AB The present invention provides compns. and methods for controlling an helminth or arthropod pest. In a preferred embodiment of the invention provided herein, the compns. comprise one of the compds. I, II, and III (X = (un)substituted cyclic ring; Y = (un)substituted alkyl, (un)substituted

alkoxy, (un)interrupted by heteroatoms; D = C, CH, CH2, O, and N; R = H, alkyl), which alter the 5-HT3 receptor of the pest. Also claimed are various esters of N-Me 8-azabicyclo[3.2.1]octan-3-ol (tropan-3-yl esters) and an assay for identifying and/or assessing a helminth and/or arthropod control compd. by detg. the ability of a candidate compd. to modulate the activity of a helminth or arthropod 5-HT3 receptor.

IT **500231-10-7**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(amino acid sequence; Caenorhabditis elegans 5-HT3 receptor; agonists and antagonists of 5-HT3 receptors of invertebrates as pesticides)

REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:290302 CAPLUS
DOCUMENT NUMBER: 136:289776
TITLE: The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens
AUTHOR(S): Slesarev, Alexei I.; Mezhevaya, Katja V.; Makarova, Kira S.; Polushin, Nikolai N.; Shcherbinina, Olga V.; Shakhova, Vera V.; Belova, Galina I.; Aravind, L.; Natale, Darren A.; Rogozin, Igor B.; Tatusov, Roman L.; Wolf, Yuri I.; Stetter, Karl O.; Malykh, Andrei G.; Koonin, Eugene V.; Kozyavkin, Sergei A.
CORPORATE SOURCE: Fidelity Systems, Gaithersburg, MD, 20879, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2002), 99(7), 4644-4649
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The complete 1,694,969-nucleotide sequence of the GC-rich genome of Methanopyrus kandleri was detd. by using a whole direct genome sequencing approach. This approach is based on unlinking of genomic DNA with the ThermoFidelase version of M. kandleri topoisomerase V and cycle sequencing directed by 2'-modified oligonucleotides (Fimers). Sequencing redundancy (3.3-fold) was sufficient to assemble the genome with less than one error per 40 kb. Using a combination of sequence database searches and coding potential prediction, 1692 protein-coding genes and 39 genes for structural RNAs were identified. M. kandleri proteins show an unusually high content of neg. charged amino acids, which might be an adaptation to the high intracellular salinity. Previous phylogenetic anal. of 16S RNA suggested that M. kandleri belonged to a very deep branch, close to the root of the archaeal tree. However, genome comparisons indicate that, in both trees constructed using concatenated alignments of ribosomal proteins and trees based on gene content, M. kandleri consistently groups with other archaeal methanogens. M. kandleri shares the set of genes implicated in methanogenesis and, in part, its operon organization with Methanococcus jannaschii and Methanothermobacter thermoautotrophicum. These findings indicate that archaeal methanogens are monophyletic. A distinctive feature of M. kandleri is the paucity of proteins involved in signaling and regulation of gene expression. Also, M. kandleri appears to have fewer genes acquired via lateral transfer than other archaea. These features might reflect the extreme habitat of this organism. The sequence is deposited in GenBank under Accession No. AE009439.

IT **406671-25-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanopyrus kandleri AV19 and monophyly of archaeal methanogens)

REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2001:618161 CAPLUS
DOCUMENT NUMBER: 135:191974
TITLE: 5HT3 receptors of nematodes, polynucleotide molecules encoding same, and their antagonists
INVENTOR(S): Trowell, Stephen Charles; Dumancic, Mira Maria; Liao, Chunyan; East, Peter David
PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organisation, Australia
SOURCE: PCT Int. Appl., 74 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001061000	A1	20010823	WO 2001-AU150	20010215
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001033491	A5	20010827	AU 2001-33491	20010215
EP 1261707	A1	20021204	EP 2001-905492	20010215
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2003523205	T2	20030805	JP 2001-560370	20010215

PRIORITY APPLN. INFO.: AU 2000-5634 A 20000215
WO 2001-AU150 W 20010215

AB Invertebrate 5-HT3 receptors, esp. from the nematode Caenorhabditis elegans, and polynucleotide mols. encoding same are disclosed. Pharmacol. identification of the 5-HT3 receptor in C. elegans shows that it is responsible for controlling the rate and strength of pharyngeal pumping. The 5-HT3-selective antagonist MDL7222 is nematicidal for C. elegans and insecticidal for the sucking insect pest Myzus persicae and antifeedant for the chewing insect pest Helicoverpa armigera. The receptors and polynucleotide mols. may be used in assays to identify and/or assess candidate compds. for use as nematicidal, insecticidal, and/or other pesticidal use.

IT **356608-55-4**
RL: AGR (Agricultural use); BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)
(amino acid sequence; 5HT3 receptors of nematodes, polynucleotide mols. encoding same, and their antagonists)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2001:385842 CAPLUS
DOCUMENT NUMBER: 135:1234
TITLE: Eicosapentaenoic acid biosynthetic production by recombinant marine cyanobacteria, Synechococcus
INVENTOR(S): Yazawa, Kazuyoshi; Yu, Reiko; Yamada, Akiko; Matsunaga, Sunao; Takeyama, Haruko; Kurane, Ryuichiro
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan; Bioindustry Association; Ministry of Economy, Trade and Industry;

Searched by Barb O'Bryen, STIC 308-4291

SOURCE: National Industrial Research Institute
Jpn. Kokai Tokkyo Koho, 62 pp.
CODEN: JKXXAF

DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2001145490	A2	20010529	JP 1999-329169	19991119

PRIORITY APPLN. INFO.: JP 1999-329169 19991119

AB Transformation of marine cyanobacteria with eicosapentaenoic acid (EPA) synthetic enzyme gene cluster for EPA biosynthetic prodn., is disclosed. Plasmid vectors contg. the gene cluster are claimed. The eicosapentaenoic acid (EPA) synthesis gene cluster from an EPA-producing bacterium, Shewanella sp. SCRC-2738, was cloned into a broad-host range vector, pJRD215, and then introduced into a marine cyanobacterium, Synechococcus sp. NKBG15041c, by conjugation. The transconjugant cyanobacteria produced 3.7 .+-. 0.2% (2.24 .+-. 0.13 mg/L) EPA (n-3) and 2.5 .+-. 0.2% (1.49 .+-. 0.06 mg/L) eicosatetraenoic acid (n-3) of the total fatty acids when the cells were cultured at 23.degree.C at a light intensity of 1,000-1,500 Lx. The EPA and eicosatetraenoic acid contents of the cells were increased to 4.6 .+-. 0.6% (3.86 .+-. 1.11 mg/L) and 4.7 .+-. 0.3% (3.86 .+-. 0.82 mg/L), and 7.5 .+-. 0.3% (1.76 .+-. 0.10 mg/L) and 5.1 .+-. 0.2% (1.19 .+-. 0.06 mg/L) when they were cultured at low temp. (18.degree.C) and at lower light intensity (40 Lx), resp.

IT **342056-52-4P**
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; eicosapentaenoic acid prodn. by recombinant Synechococcus)

L4 ANSWER 11 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2001:526443 CAPLUS
DOCUMENT NUMBER: 135:87850
TITLE: The complete genome of the crenarchaeon Sulfolobus solfataricus P2
AUTHOR(S): She, Qunxin; Singh, Rama K.; Confalonieri, Fabrice; Zivanovic, Yvan; Allard, Ghislaine; Awayez, Mariana J.; Chan-Weiher, Christina C.-Y.; Clausen, Ib Groth; Curtis, Bruce A.; De Moors, Anick; Erauso, Gael; Fletcher, Cynthia; Gordon, Paul M. K.; Heikamp-De Jong, Ineke; Jeffries, Alex C.; Kozera, Catherine J.; Medina, Nadine; Peng, Xu; Thi-Ngoc, Hoa Phan; Redder, Peter; Schenk, Margaret E.; Theriault, Cynthia; Tolstrup, Niels; Charlebois, Robert L.; Doolittle, W. Ford; Duguet, Michel; Gaasterland, Terry; Garrett, Roger A.; Ragan, Mark A.; Sensen, Christoph W.; Van der Oost, John
CORPORATE SOURCE: Microbial Genome Group, Institute of Molecular Biology, University of Copenhagen, Copenhagen, DK-1307, Den.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(14), 7835-7840
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The genome of the crenarchaeon Sulfolobus solfataricus P2 contains 2,992,245 bp on a single chromosome and encodes 2977 proteins and many RNAs. One-third of the encoded proteins have no detectable homologs in other sequenced genomes. Moreover, 40% appear to be archaeal-specific,

and only 12% and 2.3% are shared exclusively with bacteria and eukarya, resp. The genome shows a high level of plasticity with 200 diverse insertion sequence elements, many putative nonautonomous mobile elements, and evidence of integrase-mediated insertion events. There are also long clusters of regularly spaced tandem repeats. Different transfer systems are used for the uptake of inorg. and org. solutes, and a wealth of intracellular and extracellular proteases, sugar, and sulfur-metabolizing enzymes are encoded, as well as enzymes of the central metabolic pathways and motility proteins. The major metabolic electron carrier is not NADH as in bacteria and eukarya but probably ferredoxin. The essential components required for DNA replication, DNA repair and recombination, the cell cycle, transcriptional initiation and translation, but not DNA folding, show a strong eukaryal character with many archaeal-specific features. The results illustrate major differences between crenarchaea and euryarchaea, esp. for their DNA replication mechanism and cell cycle processes and their translational app. The complete annotated genome sequence is available in GenBank Accession No. AE006641.

IT **348670-68-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome of Sulfolobus solfataricus P2)

REFERENCE COUNT: 85 THERE ARE 85 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2001:576756 CAPLUS
DOCUMENT NUMBER: 135:163233
TITLE: Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum
AUTHOR(S): Nolling, Jork; Breton, Gary; Omelchenko, Marina V.; Makarova, Kira S.; Zeng, Qiandong; Gibson, Rene; Lee, Hong Mei; Dubois, Joann; Qiu, Dayong; Hitti, Joseph; Wolf, Yuri I.; Tatusov, Roman L.; Sabathe, Fabrice; Doucette-Stamm, Lynn; Soucaille, Philippe; Daly, Michael J.; Bennett, George N.; Koonin, Eugene V.; Smith, Douglas R.; Aldredge, Tyler; Ayers, Mark; Bashirzadeh, Romina; Bochner, Harry; Boivin, Mike; Bross, Susan; Bush, David; Butler, Carole; Caron, Anne; Caruso, Anthony; Cook, Robin; Daggett, Patricia; Deloughery, Craig; Egan, Jeff; Ellston, Dawna; Engelstein, Marcy; Ezedi, Johnny; Gilbert, Katie; Goyal, Anil; Guerin, Jennifer; Ho, Tay; Holtham, Kari; Joseph, Paul; Keagle, Pamela; Kozlovsky, Julia; LaPlante, Mary; LeBlanc, Gary; Lumm, Wendy; Majeski, Amy; McDougall, Steve; Mank, Philip; Mao, Jen-I.; Nocco, Diane; Patwell, Donivan; Phillips, Jonathon; Pothier, Bryan; Prabhakar, Shashi; Richterich, Peter; Rice, Philip; Rosetti, Dawn; Rossetti, Mark; Rubenfield, Marc; Sachdeva, Meena; Snell, Philip; Spadafora, Rob; Spitzer, Lia; Shimer, George; Thomann, Hans-Ulrich; Vicaire, R.; Wall, Kristen; Wang, Ying; Weinstock, Keith; Wong, Lai Peng; Wonsey, A.; Xu, Qinxue; Zhang, Liping
CORPORATE SOURCE: GTC Sequencing Center, Genome Therapeutics Corporation, Waltham, MA, 02453, USA
SOURCE: Journal of Bacteriology (2001), 183(16), 4823-4838
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The genome sequence of the solvent-producing bacterium Clostridium acetobutylicum ATCC 824 was detd. by the shotgun approach. The genome consists of a 3.94-Mb chromosome and a 192-kb megaplasmid that contains

the majority of genes responsible for solvent prodn. Comparison of C. acetobutylicum to Bacillus subtilis reveals significant local conservation of gene order, which has not been seen in comparisons of other genomes with similar, or, in some cases closer, phylogenetic proximity. This conservation allows the prediction of many previously undetected operons in both bacteria. However, the C. acetobutylicum genome also contains a significant no. of predicted operons that are shared with distantly related bacteria and archaea but not with B. subtilis. Phylogenetic anal. is compatible with the dissemination of such operons by horizontal transfer. The enzymes of the solventogenesis pathway and of the cellulosome of C. acetobutylicum comprise a new set of metabolic capacities not previously represented in the collection of complete genomes. These enzymes show a complex pattern of evolutionary affinities, emphasizing the role of lateral gene exchange in the evolution of the unique metabolic profile of the bacterium. Many of the sporulation genes identified in B. subtilis are missing in C. acetobutylicum, suggesting major differences in the sporulation process. Thus, comparative anal. reveals both significant conservation of the genome organization and pronounced differences in many systems that reflect unique adaptive strategies of the two gram-pos. bacteria. The sequence data is available in the GenBank database with Accession Nos. AE001438 and AE007513-AE007868.

IT **353881-58-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence and comparative anal. of the solvent-producing bacterium Clostridium acetobutylicum)

REFERENCE COUNT: 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 13 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2000:493686 CAPLUS
DOCUMENT NUMBER: 133:115928
TITLE: Schizochytrium polyketide synthase genes and transgenic plants for polyunsaturated long chain fatty acid production
INVENTOR(S): Facciotti, Daniel; Metz, James George; Lassner, Michael[9]
PATENT ASSIGNEE(S): Calgene, LLC, USA
SOURCE: PCT Int. Appl., 303 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000042195	A2	20000720	WO 2000-US956	20000114
WO 2000042195	A3	20000928		
W: BR, CA, IL, JP, MX				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6566583	B1	20030520	US 1999-231899	19990114
CA 2359629	AA	20000720	CA 2000-2359629	20000114
EP 1147197	A2	20011024	EP 2000-904357	20000114
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 2000008760	A	20021008	BR 2000-8760	20000114
JP 2002534123	T2	20021015	JP 2000-593752	20000114

PRIORITY APPLN. INFO.:
US 1999-231899 A 19990114
US 1997-48650P P 19970604
US 1998-90793 A2 19980604

WO 2000-US956 W 20000114

AB The present invention relates to compns. and methods for prepg. polyunsatd. long-chain fatty acids in plants, plant parts and plant cells, such as leaves, roots, fruits and seeds. Nucleic acid sequences and constructs encoding polyketide synthase (PKS)-like genes required for the polyunsatd. long-chain fatty acid prodn., including the genes responsible for eicosapentenoic acid prodn. of Shewanella putrefaciens and novel genes assocd. with the prodn. of docosahexenoic acid in Vibrio marinus are used to generate transgenic plants, plant parts and cells which contain and express one or more transgenes encoding one or more of the PKS-like genes assocd. with such long chain polyunsatd. fatty acid prodn. PKS-like genes from Schizochytrium aggregatum are also provided. Expression of the PKS-like genes in the plant system permits the large scale prodn. of polyunsatd. long-chain fatty acids such as eicosapentenoic acid and docosahexenoic acid for modification of the fatty acid profile of plants, plant parts and tissues. Manipulation of the fatty acid profiles allows for the prodn. of com. quantities of novel plant oils and products.

IT **153926-89-7**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Schizochytrium polyketide synthase genes and transgenic plants for polyunsatd. long chain fatty acid prodn.)

L4 ANSWER 14 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2000:754712 CAPLUS
DOCUMENT NUMBER: 133:330538
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302828	AA	20001006	CA 2000-2302828	20000406
EP 1055728	A2	20001129	EP 2000-303770	20000504
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-304161	20000517
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:
US 1999-121825P P 19990225
US 1999-145918P P 19990727
US 1999-145951P P 19990728
US 1999-146386P P 19990802
US 1999-146388P P 19990802
US 1999-146389P P 19990802
US 1999-147038P P 19990803
US 1999-147204P P 19990804
US 1999-147302P P 19990804
US 1999-147192P P 19990805

US 1999-147260P P 19990805
US 1999-147303P P 19990806
US 1999-147416P P 19990806
US 1999-147493P P 19990809
US 1999-147935P P 19990809
US 1999-148171P P 19990810
US 1999-148319P P 19990811
US 1999-148341P P 19990812
US 1999-148565P P 19990813
US 1999-148684P P 19990813
US 1999-123180P P 19990305
US 1999-123548P P 19990309
US 1999-125788P P 19990323
US 1999-126264P P 19990325
US 1999-126785P P 19990329
US 1999-127462P P 19990401
US 1999-128234P P 19990406
US 1999-128714P P 19990408
US 1999-129845P P 19990416
US 1999-130077P P 19990419
US 1999-130449P P 19990421
US 1999-130510P P 19990423
US 1999-130891P P 19990423
US 1999-131449P P 19990428
US 1999-132048P P 19990430
US 1999-132407P P 19990430
US 1999-132484P P 19990504
US 1999-132485P P 19990505
US 1999-132486P P 19990506
US 1999-132487P P 19990506
US 1999-132863P P 19990507
US 1999-134256P P 19990511
US 1999-134218P P 19990514
US 1999-134219P P 19990514
US 1999-134221P P 19990514
US 1999-134370P P 19990514
US 1999-134768P P 19990518
US 1999-134941P P 19990519
US 1999-135124P P 19990520
US 1999-135353P P 19990521
US 1999-135629P P 19990524
US 1999-136021P P 19990525
US 1999-136392P P 19990527
US 1999-136782P P 19990528
US 1999-137222P P 19990601
US 1999-137528P P 19990603
US 1999-137502P P 19990604
US 1999-137724P P 19990607
US 1999-138094P P 19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA13316218528Q necessitated by the large no. of index entries required to

fully index the document and publication system constraints.].

IT **303239-85-2 303239-86-3 303239-87-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L4 ANSWER 15 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2000:776252 CAPLUS
DOCUMENT NUMBER: 134:41140
TITLE: Production of eicosapentaenoic acid by a recombinant marine cyanobacterium, Synechococcus sp.
AUTHOR(S): Yu, Reiko; Yamada, Akiko; Watanabe, Kazuo; Yazawa, Kazunaga; Takeyama, Haruko; Matsunaga, Tadashi; Kurane, Ryuichiro
CORPORATE SOURCE: Sagami Chemical Research Center, Kanagawa, 229-0012, Japan
SOURCE: Lipids (2000), 35(10), 1061-1064
CODEN: LPDSAP; ISSN: 0024-4201
PUBLISHER: AOCS Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The eicosapentaenoic acid (EPA) synthesis gene cluster from an EPA-producing bacterium, Shewanella sp. SCRC-2738, was cloned into a broad-host range vector, pJRD215, and then introduced into a marine cyanobacterium, Synechococcus sp. NKBG15041c, by conjugation. The transconjugant cyanobacteria produced 3.7 .+-. 0.2% (2.24 .+-. 0.13 mg/L) EPA (n-3) and 2.5 .+-. 0.2% (1.49 .+-. 0.06 mg/L) eicosatetraenoic acid (n-3) of the total fatty acids when the cells were cultured at 23.degree.C at a light intensity of 1,000-1,500 Lx. The EPA and eicosatetraenoic acid contents of the cells were increased to 4.6 .+-. 0.6% (3.86 .+-. 1.11 mg/L) and 4.7 .+-. 0.3% (3.86 .+-. 0.82 mg/L), and 7.5 .+-. 0.3% (1.76 .+-. 0.10 mg/L) and 5.1 .+-. 0.2% (1.19 .+-. 0.06 mg/L) when they were cultured at low temp. (18.degree.C) and at lower light intensity (40 Lx), resp.
IT **153926-89-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; eicosapentaenoic acid prodn. by a recombinant Synechococcus sp.)
REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 16 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:66002 CAPLUS
DOCUMENT NUMBER: 128:98584
TITLE: Cloning of genes for 9 eicosapentaenoic acid synthesizing enzymes of Shewanella putrefaciens and expression of the genes in Escherichia coli for production of eicosapentaenoic acid
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kondo, Kiyosi; Kato, Seishi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9801565 A1 19980115 WO 1997-JP2371 19970709
W: AU, CA, JP, NO
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AU 9734583 A1 19980202 AU 1997-34583 19970709
AU 727694 B2 20001221
EP 913473 A1 19990506 EP 1997-930728 19970709
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
NO 9900083 A 19990304 NO 1999-83 19990108
PRIORITY APPLN. INFO.: JP 1996-180845 A 19960710
WO 1997-JP2371 W 19970709

AB Provided is an advantageous process for prodn. of icosapentaenoic acid (EPA), which process comprises isolation of genes coding for a group of EPA biosynthesis enzymes from Shewanella putrefaciens strain SCRC-2874 and expression of the enzymes in Escherichia coli. Upstream of open reading frame ORF2, downstream of ORF10, and ORF2 are not involved with the biosynthesis of EPA. ORF3, 6, 7, 8, and 9 are essential for the biosynthesis of EPA. EPA is useful as pharmaceuticals, agrochems., foods, and feeds.

IT **153926-89-7**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; cloning of genes for 9 eicosapentaenoic acid synthesizing enzymes of Shewanella putrefaciens and expression of genes in Escherichia coli for prodn. of eicosapentaenoic acid)

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 17 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1996:563418 CAPLUS
DOCUMENT NUMBER: 125:215689
TITLE: Cloning of genes for biosynthetic enzyme group for eicosapentaenoic acid of Shewanella putrefaciens and process for producing eicosapentaenoic acid
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kondo, Kiyosi; Kato, Seishi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 143 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9621735	A1	19960718	WO 1996-JP30	19960112
W: AU, CA, FI, NO				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2209987	AA	19960718	CA 1996-2209987	19960112
AU 9644001	A1	19960731	AU 1996-44001	19960112
JP 08242867	A2	19960924	JP 1996-3485	19960112
EP 831149	A1	19980325	EP 1996-900433	19960112
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				

PRIORITY APPLN. INFO.: JP 1995-4299 19950113
WO 1996-JP30 19960112

AB The gene for enzymes assocd. with the biosynthesis of eicosapentaenoic acid was isolated from Shewanella putrefaciens strain SCRC-2874 and characterized. It contains 9 open reading frames (ORF 2.apprx.10). Manuf. of eicosapentaenoic acid by expression of the genes in transgenic microorganisms such as Escherichia coli is claimed.

IT **153926-89-7**

RL: PRP (Properties)
(amino acid sequence; cloning of genes for biosynthetic enzyme group for eicosapentaenoic acid of Shewanella putrefaciens and process for producing eicosapentaenoic acid)

L4 ANSWER 18 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1995:569921 CAPLUS
DOCUMENT NUMBER: 123:219957
TITLE: The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution
AUTHOR(S): Gompels, U. A.; Nicholas, J.; Lawrence, G.; Jones, M.; Thomson, B. J.; Martin, M. E. D.; Efstathiou, S.; Craxton, M.; Macaulay, H. A.
CORPORATE SOURCE: Dept. Clinical Sci., London Sch. Hygiene and Tropical Med., London, WC1E 7HT, UK
SOURCE: Virology (1995), 209(1), 29-51
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete DNA sequence was detd. for strain U1102 of human herpesvirus-6, a CD4+ T-lymphotropic virus with disease assocns. in immunodeficient settings and a possible complicating factor in AIDS. The genome is 159,321 bp in size, has a base compn. of 43% G + C, and contains 119 open reading frames. The overall structure is 143 kb bounded by 8 kb of direct repeats, DRL (left) and DRR (right), contg. 0.35 kb of terminal and junctional arrays of human telomere-like simple repeats. Since eight open reading frames are duplicated in the repeats, six span repetitive elements and three are spliced, the genome is considered to contain 102 sep. genes likely to encode protein. The genes are arranged colinearly with those in the genome of the previously sequenced betaherpesvirus, human cytomegalovirus, and has a distinct arrangement of conserved genes relative to the sequenced gammaherpesviruses, herpesvirus saimiri and Epstein-Barr virus, and the alphaherpesviruses, equine herpesvirus-1, varicella-zoster virus, and herpes simplex virus. Comparisons of predicted amino acid sequences allowed the functions of many human herpesvirus-6 encoded proteins to be assigned and showed the closest relation in overall no. and similarity to human cytomegalovirus products, with approx. 67% homologous proteins as compared to the 21% identified in all herpesviruses. The features of the conserved genes and their relative order suggested a general scheme for divergence among these herpesvirus lineages. In addn. to the "core" conserved genes, the genome contains four distinct gene families which may be involved in immune evasion and persistence in immune cells: two have similarity to the "chemokine" chemotactic/proinflammatory family of cytokines, one to their peptide G-protein-coupled receptors, and a fourth to the Ig superfamily.
IT **167975-38-4**
RL: PRP (Properties)
(amino acid sequence; DNA and encoded peptide sequences of human herpesvirus-6)

L4 ANSWER 19 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1994:184295 CAPLUS
DOCUMENT NUMBER: 120:184295
TITLE: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions
AUTHOR(S): Nicholas, John; Martin, Michelle E. D.
CORPORATE SOURCE: Johns Hopkins Oncol. Cent., Baltimore, MD, 21231, USA
SOURCE: Journal of Virology (1994), 68(2), 597-610
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal

Searched by Barb O'Bryen, STIC 308-4291

LANGUAGE: English

AB Human herpesvirus 6 (HHV-6) is prevalent in the human population, with primary infection occurring early in life. Its predominant CD4+ T-lymphocyte tropism, its ability to activate human immunodeficiency virus type 1 (HIV-1) gene expression in vitro, and its upregulation of CD4 expression has led to speculation that HHV-6 may act as a pos. cofactor in the progression of HIV infection to AIDS in individuals infected with both viruses. Previous sequencing studies of restricted regions of the 161.5-kbp genome of HHV-6 have demonstrated unequivocally that it is a member of the betaherpesvirus subgroup and have indicated that the HHV-6 genome is generally collinear with the unique long (UL) component of human cytomegalovirus (HCMV). This report extended the sequencing studies by detg. the primary structure of 38.5-kbp of the HHV-6 genome (genomic position 21.0 to 59.6 kbp). Within the sequenced region lie 31 open reading frames, 20 of which are homologous to positional counterparts in HCMV. Of particular significance is the identification of homologs of the HCMV UL36-38 and US22-type genes, which have been shown to encode transactivating proteins. DNA sequences encoding these HHV-6 homologs were able to transactivate HIV-1 long terminal repeat-directed chloramphenicol acetyltransferase expression in cotransfection assays, thus demonstrating functional as well as structural conservation of these betaherpesvirus-specific gene products. The data confirm the close relationship between HHV-6 and HCMV and possibly also in the interactions between HHV-6 and HIV in dually infected cells.

IT **153676-37-0**, Genbank L25528-derived protein
RL: PRP (Properties)
(amino acid sequence of)

L4 ANSWER 20 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1994:211508 CAPLUS
DOCUMENT NUMBER: 120:211508
TITLE: Molecular cloning of gene for eicosapentaenoic acid synthetase group of Shewanella putrefaciens
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9323545	A1	19931125	WO 1993-JP641	19930514
W: AU, CA, FI, NO, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2113557	AA	19931125	CA 1993-2113557	19930514
AU 9340881	A1	19931213	AU 1993-40881	19930514
AU 673359	B2	19961107		
JP 06046864	A2	19940222	JP 1993-135133	19930514
EP 594868	A1	19940504	EP 1993-910344	19930514
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
FI 9400203	A	19940314	FI 1994-203	19940114
NO 9400146	A	19940314	NO 1994-146	19940114

PRIORITY APPLN. INFO.: JP 1992-147945 19920515
WO 1993-JP641 19930514

AB A gene for eicosapentaenoic acid (I) synthetase group of microorganisms such as Shewanella, Pseudomonas, or Alteromonas can be used for mass prodn. of I by expression of the gene in a host. I is useful as medicine, pesticide, food, feed, etc. A gene encoding I synthetase group was cloned from Shewanella putrefaciens SCRS-2874 using cosmid pWE15 and

characterized. Clone pEPA contg. a 37913-base genomic DNA comprised of 8 open reading frames (ORF) was disclosed and the amino acid sequences of each ORF were deduced. Escherichia coli transformed with pEPA was also given.

IT **153926-89-7**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of)

L4 ANSWER 21 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1993:185121 CAPLUS
DOCUMENT NUMBER: 118:185121
TITLE: Manufacture of epitopes of protein p100 of human herpesvirus type 6 for diagnostic or therapeutic uses
INVENTOR(S): Neipel, Frank; Fleckenstein, Bernhard
PATENT ASSIGNEE(S): Behringwerke AG, Germany; Dade Behring Marburg GmbH
SOURCE: Eur. Pat. Appl., 25 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 524421	A1	19930127	EP 1992-110047	19920615
EP 524421	B1	20030326		
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, PT, SE				
AT 235553	E	20030415	AT 1992-110047	19920615
CA 2073282	AA	19930109	CA 1992-2073282	19920707
AU 9219455	A1	19930114	AU 1992-19455	19920707
AU 666482	B2	19960215		
JP 06113858	A2	19940426	JP 1992-204414	19920708
JP 3425164	B2	20030707		
US 5814475	A	19980929	US 1994-266311	19940627
US 5827519	A	19981027	US 1995-467527	19950606
US 6174685	B1	20010116	US 1995-467528	19950606

PRIORITY APPLN. INFO.: EP 1991-111338 A 19910708
US 1992-908041 B1 19920706
US 1993-126435 B1 19930924
US 1994-266311 A3 19940627

AB Fragments of the gene for the major capsid protein p100 of human herpesvirus 6 (HHV6) are used to manuf. epitopes for diagnostic differentiation of HHV6 and human cytomegalovirus and for therapeutic applications. The use of the epitope in immunoassays to identify HHV6 infection was demonstrated.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, manuf. of epitopes of)

L4 ANSWER 22 OF 26 USPATFULL on STN
ACCESSION NUMBER: 2001:7853 USPATFULL
TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA sequences, their preparation and use
INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of
PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6174685	B1	20010116

Searched by Barb O'Bryen, STIC 308-4291

APPLICATION INFO.: US 1995-467528 19950606 (8)
RELATED APPLN. INFO.: Division of Ser. No. US 1994-266311, filed on 27 Jun 1994 Continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned Continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ketter, James
ASSISTANT EXAMINER: Yucel, Irem
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 6
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 333
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further relates to antibodies directed to them and to the corresponding DNA sequences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6) (amino acid sequence of, complete, manuf. of epitopes of)

L4 ANSWER 23 OF 26 USPATFULL on STN
ACCESSION NUMBER: 1998:131399 USPATFULL
TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA sequences, their preparation and use
INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of
PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5827519		19981027
APPLICATION INFO.:	US 1995-467527		19950606 (8)

RELATED APPLN. INFO.: Division of Ser. No. US 1994-266311, filed on 27 Jun 1994 which is a continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned which is a continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ketter, James
ASSISTANT EXAMINER: Brusca, John S.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 8
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 647
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further

relates to antibodies directed to them and to the corresponding DNA sequences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6) (amino acid sequence of, complete, manuf. of epitopes of)

L4 ANSWER 24 OF 26 USPATFULL on STN

ACCESSION NUMBER: 1998:118997 USPATFULL

TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA seqences, their preparation and use

INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of

PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5814475		19980929
APPLICATION INFO.:	US 1994-266311		19940627 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned which is a continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Stanton, Brian R.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 646
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further relates to antibodies directed to them and to the corresponding DNA seqúences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6) (amino acid sequence of, complete, manuf. of epitopes of)

L4 ANSWER 25 OF 26 MEDLINE on STN DUPLICATE 6

ACCESSION NUMBER: 94025558 MEDLINE
DOCUMENT NUMBER: 94025558 PubMed ID: 7692666

TITLE: Human herpesvirus-6 glycoprotein H and L homologs are components of the gp100 complex and the gH external domain is the target for neutralizing monoclonal antibodies.

AUTHOR: Liu D X; Gompels U A; Foa-Tomasi L; Campadelli-Fiume G

CORPORATE SOURCE: Department of Medicine, University of Cambridge, United Kingdom.

SOURCE: VIROLOGY, (1993 Nov) 197 (1) 12-22.
Journal code: 0110674. ISSN: 0042-6822.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19970203
Entered Medline: 19931122

ABSTRACT:
Previous studies have shown that monoclonal antibody (MAb) 2E4 neutralizes infectivity of human herpesvirus-6 (HHV-6) and also inhibits virus-induced T-lymphocyte syncytia formation. Here we characterize two additional MAbs, 1D3 and 5E7, which have similar properties, and identify the glycoprotein targets. The MAbs could immunoprecipitate and immunofluorescence glycoprotein from both A and B variant strain groups of HHV-6. In reactions with infected cells the MAbs immunoprecipitated a complex of glycoproteins, the "gp100" complex, composed of a major glycoprotein species of 100,000 M(r) and minor components of 80,000 M(r) and 32,000 M(r). We show that the 100,000 M(r) product and most likely the 80,000 M(r) correspond to the HHV-6 homologue of herpes simplex virus-1 (HSV-1) glycoprotein H (gH) while the 32,000 M(r) species corresponds to the glycoprotein L (gL) equivalent. All three MAbs could specifically immunoprecipitate either gH expressed on its own in fibroblasts or a complex of gH and gL co-expressed, but could not immunoprecipitate gL expressed on its own. Consistent with these results, the MAbs could recognize gH in an immunofluorescence assay but not gL. Therefore although the MAbs recognized the complex of glycoproteins, they appeared specific for gH. The HHV-6 glycoproteins were produced in a transient expression system induced by T7-vaccinia virus. Immunoprecipitations were carried out in comparisons with an "epitope-tagged" gH, a recombinant glycoprotein designed to contain at the N-terminus the linear epitope for MAb LP14, raised originally against HSV-1 glycoprotein gD. The epitope-tagged gH was also used as a positive control in determining the domain of HHV-6 gH to which MAbs 2E4, 1D3 and 5E7 were directed. Two gH deletions were constructed, one deleting sequences which may serve as a transmembrane and cytoplasmic anchor domains, the second deleting also part of the external domain. MAb LP14 could immunoprecipitate both HHV-6 gH deletions but the gp100 MAbs recognized only the full-length product or the intact external domain minus the transmembrane and cytoplasmic domains. This indicated the epitopes for these MAbs are contained in the external domain of gH, consistent with the MAbs action in neutralization of virion infectivity and inhibition of virus to cell spread by T-lymphocyte fusion.

CONTROLLED TERM: Check Tags: Animal; Comparative Study; Human; Support, Non-U.S. Gov't
Amino Acid Sequence
*Antibodies, Monoclonal: ME, metabolism
Antigen-Antibody Reactions
Base Sequence
Cell Line
DNA Primers
Electrophoresis, Polyacrylamide Gel
Epitopes: AN, analysis
Fluorescent Antibody Technique
Glycoproteins: IM, immunology
Glycoproteins: IP, isolation & purification
*Glycoproteins: ME, metabolism
Herpesvirus 6, Human: IM, immunology
*Herpesvirus 6, Human: ME, metabolism
Mice
Mice, Inbred BALB C: IM, immunology
Molecular Sequence Data
Molecular Weight
Mutagenesis, Site-Directed
Neutralization Tests
Polymerase Chain Reaction
Sequence Deletion
Sequence Homology, Amino Acid
Transfection

Viral Envelope Proteins: IM, immunology
Viral Envelope Proteins: IP, isolation & purification
*Viral Envelope Proteins: ME, metabolism
Viral Proteins: IM, immunology
Viral Proteins: IP, isolation & purification
*Viral Proteins: ME, metabolism

CAS REGISTRY NO.: 142985-75-9 (glycoprotein H, herpesvirus 6);
147338-03-2 (human herpesvirus 6 protein p100)

CHEMICAL NAME: 0 (Antibodies, Monoclonal); 0 (DNA Primers); 0 (Epitopes); 0 (Glycoproteins); 0 (Viral Envelope Proteins); 0 (Viral Proteins)

L4 ANSWER 26 OF 26 MEDLINE on STN
ACCESSION NUMBER: 94018614 MEDLINE
DOCUMENT NUMBER: 94018614 PubMed ID: 8412672
TITLE: S-layer protein from Thermus thermophilus HB8 assembles into porin-like structures.
AUTHOR: Caston J R; Berenguer J; de Pedro M A; Carrascosa J L
CORPORATE SOURCE: Centro de Biologia Molecular (CSIC-UAM), Universidad Autonoma de Madrid, Cantoblanco Spain.
SOURCE: MOLECULAR MICROBIOLOGY, (1993 Jul) 9 (1) 65-75.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19950206
Entered Medline: 19931104

ABSTRACT:
The cells of the extreme thermophile Thermus thermophilus are surrounded by a regular layer (S-layer) built up by a protein with an apparent molecular mass of 100 kDa (P100). From purified membrane fractions, three different class of two-dimensional crystals can be obtained by following alternative extractive procedures. One of these crystals, with p6 symmetry, clearly represents the native S-layer detected by freeze etching on whole cells, while the other two, showing p2 and p3 symmetries respectively, closely resemble aggregates of bacterial porins. We demonstrate here by limited proteolysis and Western blotting the surprising fact that the protein component of the three crystals is the P100 protein. Our biochemical data also show how this protein forms Ca(2+)-stabilized trimers in each crystal, which support the structural analysis that points to p3 units as the common structural block in all of them, and again resembles the situation found in bacterial porins.

CONTROLLED TERM: Check Tags: Support, Non-U.S. Gov't
Blotting, Western
Calcium: ME, metabolism
Cell Fractionation
Crystallization
Edetic Acid: PD, pharmacology
Fourier Analysis
Freeze Etching
Lipids: ME, metabolism
Microscopy, Electron
Peptidoglycan: ME, metabolism
Polymers
*Protein Conformation
Thermus thermophilus: ME, metabolism
*Thermus thermophilus: UL, ultrastructure
*Viral Proteins: CH, chemistry
Viral Proteins: IP, isolation & purification
Viral Proteins: ME, metabolism

CAS REGISTRY NO.: **147338-03-2 (human herpesvirus 6 protein p100);**

CHEMICAL NAME: 60-00-4 (Edetic Acid); 7440-70-2 (Calcium) 0 (Lipids); 0 (Peptidoglycan); 0 (Polymers); 0 (Viral Proteins)

FILE 'HOME' ENTERED AT 10:57:03 ON 12 AUG 2003

1: CAA58438. U11, pp100 [Human...[gi:853990]

BLink, Links

LOCUS CAA58438 870 aa linear VRL 17-FEB-1997
DEFINITION U11, pp100 [Human herpesvirus 6].
ACCESSION CAA58438
VERSION CAA58438.1 GI:853990
DBSOURCE embl locus HHV6AGNM, accession X83413.1
KEYWORDS .
SOURCE Human herpesvirus 6
ORGANISM Human herpesvirus 6
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.

REFERENCE 1
AUTHORS Chee,M.S., Lawrence,G.L. and Barrell,B.G.
TITLE Alpha-, beta- and gammaherpesviruses encode a putative phosphotransferase
JOURNAL J. Gen. Virol. 70 (Pt 5), 1151-1160 (1989)
MEDLINE 89279291
PUBMED 2543772

REFERENCE 2
AUTHORS Lawrence,G.L., Chee,M., Craxton,M.A., Gompels,U.A., Honess,R.W. and Barrell,B.G.
TITLE Human herpesvirus 6 is closely related to human cytomegalovirus
JOURNAL J. Virol. 64 (1), 287-299 (1990)
MEDLINE 90080132
PUBMED 2152817

REFERENCE 3
AUTHORS Littler,E., Lawrence,G., Liu,M.Y., Barrell,B.G. and Arrand,J.R.
TITLE Identification, cloning, and expression of the major capsid protein gene of human herpesvirus 6
JOURNAL J. Virol. 64 (2), 714-722 (1990)
MEDLINE 90112641
PUBMED 2153237

REFERENCE 4
AUTHORS Martin,M.E., Thomson,B.J., Honess,R.W., Craxton,M.A., Gompels,U.A., Liu,M.Y., Littler,E., Arrand,J.R., Teo,I. and Jones,M.D.
TITLE The genome of human herpesvirus 6: maps of unit-length and concatemeric genomes for nine restriction endonucleases
JOURNAL J. Gen. Virol. 72 (Pt 1), 157-168 (1991)
MEDLINE 91116306
PUBMED 1846644

REFERENCE 5
AUTHORS Thomson,B.J., Efstathiou,S. and Honess,R.W.
TITLE Acquisition of the human adeno-associated virus type-2 rep gene by human herpesvirus type-6
JOURNAL Nature 351 (6321), 78-80 (1991)
MEDLINE 91226542
PUBMED 1851252

REFERENCE 6
AUTHORS Chang,C.K. and Balachandran,N.
TITLE Identification, characterization, and sequence analysis of a cDNA encoding a phosphoprotein of human herpesvirus 6
JOURNAL J. Virol. 65 (6), 2884-2894 (1991)

MEDLINE 91237802
PUBMED 1851860
REFERENCE 7
AUTHORS Teo,I.A., Griffin,B.E. and Jones,M.D.
TITLE Characterization of the DNA polymerase gene of human herpesvirus 6
JOURNAL J. Virol. 65 (9), 4670-4680 (1991)
MEDLINE 91333007
PUBMED 1651403
REFERENCE 8
AUTHORS Martin,M.E., Nicholas,J., Thomson,B.J., Newman,C. and Honess,R.W.
TITLE Identification of a transactivating function mapping to the putative immediate-early locus of human herpesvirus 6
JOURNAL J. Virol. 65 (10), 5381-5390 (1991)
MEDLINE 91374590
PUBMED 1654446
REFERENCE 9
AUTHORS Geng,Y.Q., Chandran,B., Josephs,S.F. and Wood,C.
TITLE Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type 1 promoter
JOURNAL J. Virol. 66 (3), 1564-1570 (1992)
MEDLINE 92148942
PUBMED 1310766
REFERENCE 10
AUTHORS Neipel,F., Ellinger,K. and Fleckenstein,B.
TITLE Gene for the major antigenic structural protein (p100) of human herpesvirus 6
JOURNAL J. Virol. 66 (6), 3918-3924 (1992)
MEDLINE 92260671
PUBMED 1374813
REFERENCE 11
AUTHORS Thomson,B.J. and Honess,R.W.
TITLE The right end of the unique region of the genome of human herpesvirus 6 U1102 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene family
JOURNAL J. Gen. Virol. 73 (Pt 7), 1649-1660 (1992)
MEDLINE 92333248
PUBMED 1321205
REFERENCE 12
AUTHORS Efstathiou,S., Lawrence,G.L., Brown,C.M. and Barrell,B.G.
TITLE Identification of homologues to the human cytomegalovirus US22 gene family in human herpesvirus 6
JOURNAL J. Gen. Virol. 73 (Pt 7), 1661-1671 (1992)
MEDLINE 92333249
PUBMED 1321206
REFERENCE 13
AUTHORS Gompels,U.A., Carss,A.L., Sun,N. and Arrand,J.R.
TITLE Infectivity determinants encoded in a conserved gene block of human herpesvirus-6
JOURNAL DNA Seq. 3 (1), 25-39 (1992)
MEDLINE 93091236
PUBMED 1333836
REFERENCE 14
AUTHORS Ellinger,K., Neipel,F., Foa-Tomasi,L., Campadelli-Fiume,G. and Fleckenstein,B.
TITLE The glycoprotein B homologue of human herpesvirus 6
JOURNAL J. Gen. Virol. 74 (Pt 3), 495-500 (1993)
MEDLINE 93187613
PUBMED 8383182
REFERENCE 15
AUTHORS Gompels,U.A., Carrigan,D.R., Carss,A.L. and Arno,J.
TITLE Two groups of human herpesvirus 6 identified by sequence analyses of laboratory strains and variants from Hodgkin's lymphoma and bone marrow transplant patients

JOURNAL J. Gen. Virol. 74 (Pt 4), 613-622 (1993)
MEDLINE 93224882
PUBMED 8385692
REFERENCE 16
AUTHORS Pfeiffer,B., Berneman,Z.N., Neipel,F., Chang,C.K., Tirwatnapong,S. and Chandran,B.
TITLE Identification and mapping of the gene encoding the glycoprotein complex gp82-gp105 of human herpesvirus 6 and mapping of the neutralizing epitope recognized by monoclonal antibodies
JOURNAL J. Virol. 67 (8), 4611-4620 (1993)
MEDLINE 93323202
PUBMED 7687301
REFERENCE 17
AUTHORS Pellett,P.E., Sanchez-Martinez,D., Dominguez,G., Black,J.B., Anton,E., Greenamoyer,C. and Dambaugh,T.R.
TITLE A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain Z29: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive epitope
JOURNAL Virology 195 (2), 521-531 (1993)
MEDLINE 93331710
PUBMED 7687803
REFERENCE 18
AUTHORS Liu,D.X., Gompels,U.A., Nicholas,J. and Lelliott,C.
TITLE Identification and expression of the human herpesvirus 6 glycoprotein H and interaction with an accessory 40K glycoprotein
JOURNAL J. Gen. Virol. 74 (Pt 9), 1847-1857 (1993)
MEDLINE 93389439
PUBMED 8397282
REFERENCE 19
AUTHORS Qian,G., Wood,C. and Chandran,B.
TITLE Identification and characterization of glycoprotein gH of human herpesvirus-6
JOURNAL J. Virol. 194, 380-386 (1993)
REFERENCE 20
AUTHORS Liu,D.X., Gompels,U.A., Foa-Tomasi,L. and Campadelli-Fiume,G.
TITLE Human herpesvirus-6 glycoprotein H and L homologs are components of the gp100 complex and the gH external domain is the target for neutralizing monoclonal antibodies
JOURNAL Virology 197 (1), 12-22 (1993)
MEDLINE 94025558
PUBMED 7692666
REFERENCE 21
AUTHORS Jones,M.D. and Teo,I.A.
TITLE Identification and analysis of the transport/capsid assembly protein (tp/cap) gene of human herpesvirus-6 (HHV6)
JOURNAL Virology 197 (1), 449-454 (1993)
MEDLINE 94025598
PUBMED 8212582
REFERENCE 22
AUTHORS Dewhurst,S., Dollard,S.C., Pellett,P.E. and Dambaugh,T.R.
TITLE Identification of a lytic-phase origin of DNA replication in human herpesvirus 6B strain Z29
JOURNAL J. Virol. 67 (12), 7680-7683 (1993)
MEDLINE 94047392
PUBMED 8230490
REFERENCE 23
AUTHORS Nicholas,J. and Martin,M.E.
TITLE Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions
JOURNAL J. Virol. 68 (2), 597-610 (1994)
MEDLINE 94118404
PUBMED 8289364
REFERENCE 24

AUTHORS Zhou,Y., Chang,C.K., Qian,G., Chandran,B. and Wood,C.
TITLE trans-activation of the HIV promoter by a cDNA and its genomic clones of human herpesvirus-6
JOURNAL Virology 199 (2), 311-322 (1994)
MEDLINE 94167865
PUBMED 8122364
REFERENCE 25
AUTHORS Thompson,J., Choudhury,S., Kashanchi,F., Doniger,J., Berneman,Z., Frenkel,N. and Rosenthal,L.J.
TITLE A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates HIV-1
JOURNAL Oncogene 9 (4), 1167-1175 (1994)
MEDLINE 94181269
PUBMED 8134119
REFERENCE 26
AUTHORS Schiewe,U., Neipel,F., Schreiner,D. and Fleckenstein,B.
TITLE Structure and transcription of an immediate-early region in the human herpesvirus 6 genome
JOURNAL J. Virol. 68 (5), 2978-2985 (1994)
MEDLINE 94202284
PUBMED 8151768
REFERENCE 27
AUTHORS Thomson,B.J., Dewhurst,S. and Gray,D.
TITLE Structure and heterogeneity of the a sequences of human herpesvirus 6 strain variants U1102 and Z29 and identification of human telomeric repeat sequences at the genomic termini
JOURNAL J. Virol. 68 (5), 3007-3014 (1994)
MEDLINE 94202288
PUBMED 8151770
REFERENCE 28
AUTHORS Inoue,N., Dambaugh,T.R., Rapp,J.C. and Pellett,P.E.
TITLE Alphaherpesvirus origin-binding protein homolog encoded by human herpesvirus 6B, a betaherpesvirus, binds to nucleotide sequences that are similar to ori regions of alphaherpesviruses
JOURNAL J. Virol. 68 (7), 4126-4136 (1994)
MEDLINE 94267872
PUBMED 8207791
REFERENCE 29
AUTHORS Thomson,B.J., Weindler,F.W., Gray,D., Schwaab,V. and Heilbronn,R.
TITLE Human herpesvirus 6 (HHV-6) is a helper virus for adeno-associated virus type 2 (AAV-2) and the AAV-2 rep gene homologue in HHV-6 can mediate AAV-2 DNA replication and regulate gene expression
JOURNAL Virology 204 (1), 304-311 (1994)
MEDLINE 94378506
PUBMED 8091661
REFERENCE 30
AUTHORS Lawrence,G.L., Nicholas,J. and Barrell,B.G.
TITLE Human herpesvirus 6 (strain U1102) encodes homologues of the conserved herpesvirus glycoprotein gM and the alphaherpesvirus origin-binding protein
JOURNAL J. Gen. Virol. (1994) In press
REFERENCE 31
AUTHORS Gompels,U.A. and Macaulay,H.A.
TITLE Characterization of human telomeric repeat sequences from human herpesvirus 6 and relationship to replication
JOURNAL J. Gen. Virol. 76 (Pt 2), 451-458 (1995)
MEDLINE 95146989
PUBMED 7844567
REFERENCE 32 (residues 1 to 870)
AUTHORS Gompels,U.A., Nicholas,J., Lawrence,G., Jones,M., Thomson,B.J., Martin,M.E., Efstathiou,S., Craxton,M. and Macaulay,H.A.
TITLE The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution
JOURNAL Virology 209 (1), 29-51 (1995)
MEDLINE 95266321

```
   PUBMED   7747482
REFERENCE   33
  AUTHORS   Nicholas,J.
  TITLE     Nucleotide sequence of a 21-kilobase-pair region of the genome of
            human herpesvirus-6 containing homologues of human cytomegalovirus
            major immediate-early and replication genes
  JOURNAL   Unpublished
REFERENCE   34
  AUTHORS   Gompels,U.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-1994) U.A. Gompels, Viral Pathogenesis Unit,
            Department of Clinical Sciences, London School of Hygiene and
            Tropical Medicine, University of London, Keppel Street, London WC1E
            7HT, UK
  REMARK    (1-159321)
FEATURES             Location/Qualifiers
     source          1..870
                     /organism="Human herpesvirus 6"
                     /virion
                     /strain="U1102, variant A"
                     /isolate="U1102"
                     /db_xref="taxon:10368"
                     /note="complete DNA sequence, from plasmid, phage and
                     cosmid cloned DNA described in [1], [32]"
     Protein         1..870
                     /product="U11, pp100"
                     /function="major antigenic structural protein; basic
                     phosphoprotein"
     CDS             1..870
                     /gene="U11"
                     /coded_by="complement(X83413.1:18966..21578)"
                     /note="old name PILF1; HCMV UL32 homologue"
                     /citation=[10]
                     /citation=[17]
                     /citation=[32]
                     /label=U11
                     /db_xref="GOA:Q00701"
                     /db_xref="SWISS-PROT:Q00701"
ORIGIN
        1 mdlqrhpipf awldrdkver ltdflsnler ldnvdlrehp hvtnscvvre gddvddlktl
       61 ynllvlwlmy hyvlskrkpd ynaiwqditk lqsvvneyln skglnkgife nmftnkekfe
      121 sqfsdinral lrlgnfikwg snvaidtpyv nltaedssei ennlqdaekn mlwytvynin
      181 dpwdengyli tsinkliylg klflaltqsw sklekvamsq ivitqnhlsg hlrrhdnfni
      241 vyshrvlqtp ltgqrvesfl kiitsdydii ksslesheas kafsmseigp nslmdfvplr
      301 gdihsnltlp smsidtkkss ldparlkksn srsldsflrm qrqpkfleld svdnagekil
      361 lkeatlggen vkattpassv slmsgvesps sftstnldlp lssftstnld lrdkshgnyk
      421 igpsgildfn vkfppnaqln tngvdllqdk tsigspssgi tdvvngfanl nlhqnksnvs
      481 ppwsrntaan adfldpvhrf vpeqtgtpfv lnnsdvagse akhttystet gvsprnvfli
      541 kdlrgkdgfr kqkqsdipks ltkerndkai mhsrevtgds gdatetvgar nspalrkikq
      601 andffaglnk kndrdvlrgg kgnskdlhsg gnakkkemsg kfnddkemtr ngqepsrslm
      661 gdarnagdeq yiqaglgqrv nnllsqftnl islgekgied ilqnqrgtel klatenksgr
      721 eseeanveki levsnpqdmf knfrlqndld svqspfrlpd adlsreldsa sfkdaldlkl
      781 pgngereidl alekvkvget etsdlkvgqd esfvpaqlmk vetpeekddi ieqmvlrirq
      841 dgetdentvs gpgvaesldi eakgesaias
//
```

☐ 1: AAA81080. Hypothetical prot...[gi:21392559] BLink, Domains, Links

```
LOCUS       AAA81080                672 aa            linear   INV 13-JAN-2003
DEFINITION  Hypothetical protein F18G5.4 [Caenorhabditis elegans].
ACCESSION   AAA81080
VERSION     AAA81080.2  GI:21392559
DBSOURCE    accession U39855.1
KEYWORDS    .
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Genome sequence of the nematode C. elegans: a platform for
            investigating biology. The C. elegans Sequencing Consortium
  JOURNAL   Science 282 (5396), 2012-2018 (1998)
  MEDLINE   99069613
   PUBMED   9851916
REFERENCE   2  (residues 1 to 672)
  AUTHORS   Favello,A.
  TITLE     The sequence of C. elegans cosmid F18G5
  JOURNAL   Unpublished (2001)
REFERENCE   3  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   4  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAY-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   5  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   6  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-NOV-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   7  (residues 1 to 672)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-2003) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
```

COMMENT On Jun 12, 2002 this sequence version replaced gi:1055091.
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

For a graphical representation of this cosmid sequence and its analysis see:
http://www.wormbase.org/db/seq/sequence?name=F18G5;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is C35B8, 1765 bp overlap; the 3' cosmid is B0416, 200 bp overlap. Actual start of this cosmid is at base position 1762 of F18G5; actual end is at 5185 of B0416.

NOTES:

Coding seqences below are the result of integration and manual review of the following data : computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
Method: conceptual translation.

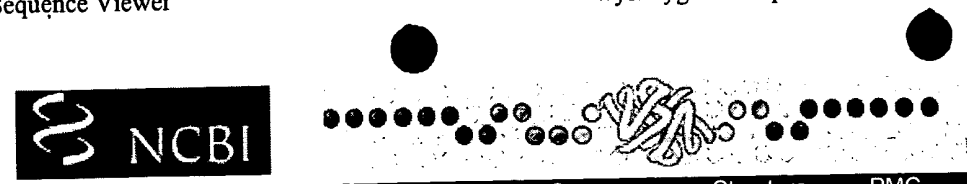
FEATURES	Location/Qualifiers
source	1..672
	/organism="Caenorhabditis elegans"
	/strain="Bristol N2"
	/db_xref="taxon:6239"
	/chromosome="X"
	/clone="F18G5"
Protein	1..672
	/product="Hypothetical protein F18G5.4"
CDS	1..672
	/gene="F18G5.4"
	/standard_name="F18G5.4"
	/coded_by="complement(join(U39855.1:1621..1737,
	U39855.1:2357..2473,U39855.1:2522..2644,
	U39855.1:2689..2820,U39855.1:2973..3178,
	U39855.1:3378..3546,U39855.1:3718..3951,
	U39855.1:3996..4134,U39855.1:6360..6514,
	U39855.1:6831..6976,U39855.1:7691..7833,

```
                     U39855.1:8325..8662))"
                     /note="contains similarity to Pfam domains PF02931
                     (Neurotransmitter-gated ion-channel ligand binding
                     domain), PF02932 (Neurotransmitter-gated ion-channel
                     transmembrane region); coded for by the following C.
                     elegans cDNAs: yk29d10.3, yk29d10.5, yk1356d06.5,
                     yk1100g12.3, yk1356d06.3"
                     /db_xref="WormBase:F18G5.4"
ORIGIN
        1 mkhvaslahc ffhlgrrclk lrphkleepr hrsklvrral lplllhsfaa ffflfcapfh
       61 titfalhity vrredlllll plciccapah hprsfsnwll kqsvqstgpq fppkfqkphn
      121 eentigtitk fapsvqeqhs savipmphfd qnrleqalri kgsidgteea lyrslldhtv
      181 yekdvrpcih hsqptnvtfg fllnqivemd ernqalttrs wlninwmdpr lswneslwse
      241 ikaiyiphar iwkpdiilvn naireyyasl vstdvmvtsd gnvtwlfsal frsscpirvr
      301 yypfddqqcd lkfaswshdi teinlglntd kgdlssymnn sefdlvdmta vrevvtfpsd
      361 tnsdwpiivi rihmhrrplf yvfnhivpcv lissmavlgf lmppetgeki nmiittllsm
      421 gvylqsites ipptsegvpl igmyyvssll mvclatcvnv itlnmhrnga anqgrhvpaw
      481 mqkwilgyla tfmrmsirep dsiallkasq skkstirrss ilrdlkrvkn msnvrakske
      541 qnanrececm dplvhiyaes imsclaadtk pmngstired fasestflgr vvsdgimpri
      601 sassnsvlte fetrfrrilk rvyrslqqhe ireeilders riqcsgnnlh lslidfyyvf
      661 falqhcsqss as
//
```

1: AAA46012. p100...[gi:330674]

BLink, Links

```
LOCUS       AAA46012                  870 aa            linear   VRL 02-AUG-1993
DEFINITION  p100.
ACCESSION   AAA46012
VERSION     AAA46012.1  GI:330674
DBSOURCE    locus HS6P100A accession M87287.1
KEYWORDS    .
SOURCE      Human herpesvirus 6
  ORGANISM  Human herpesvirus 6
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Betaherpesvirinae; Roseolovirus.
REFERENCE   1  (residues 1 to 870)
  AUTHORS   Neipel,F., Ellinger,K. and Fleckenstein,B.
  TITLE     Gene for the major antigenic structural protein (p100) of human
            herpesvirus 6
  JOURNAL   J. Virol. 66 (6), 3918-3924 (1992)
  MEDLINE   92260671
   PUBMED   1374813
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..870
                     /organism="Human herpesvirus 6"
                     /db_xref="taxon:10368"
     Protein         1..870
                     /name="p100"
     CDS             1..870
                     /gene="p100"
                     /coded_by="M87287.1:639..3251"
ORIGIN
        1 mdlqrhpipf awldrdkver ltdflsnler ldnvdlrehp hvtnscvvre gddvddlktl
       61 ynllvlwlmy hyvlskrkpd ynaiwqditk lqsvvneyln skglnkgife nmftnkekfe
      121 sqfsdinral lrlgnfikwg snvaidtpyv nltaedssei ennlqdaekn mlwytvynin
      181 dpwdengyli tsinkliylg klflaltqsw sklekvamsq ivitqhhlsg hlrrhdnfni
      241 vyshrvlqtp ltgqrvesfl kiitsdydii ksslesheas kafsmseigp nslmdfvplr
      301 gdihsnltlp smsidtkkss ldparlkksn srsldsflrm qrqpkfleld svdnagekil
      361 lkeatlggen vkattpassv slmsgvesps sftstnldlp lssftstnld lrdkshgnyk
      421 igpsgildfn vkfppnaqln tngvdllqdk tsigspssgi tdvvngfanl nlhqnksnvs
      481 ppwsrntaan adfldpvhrf vpeqtgtpfv lnnsdvagse akhttystet gvsprnvfli
      541 kdlrgkdgfr kqkqsdipks ltkerndkai mhsrevtgds gdatetvgar nspalrkikq
      601 andffaglnk kndrdvlrgg kgnskdlhsg gnakkkemsg kfnddkemtr ngqepsrslm
      661 gdarnagdeq yiqaglgqrv nnllsqftnl islgekgied ilqnqrgtel klatenksgr
      721 eseeanveki levsnpqdmf knfrlqndld svqspfrlpd adlsreldsa sfkdaldlkl
      781 pgngereidl alekvkvget etsdlkvgqd esfvpaqlmk vetpeekddi ieqmvlrirq
      841 dgetdentvs gpgvaesldi eakgesaias
//
```



1: BAB17787. mucin [Rattus nor...[gi:11138240]

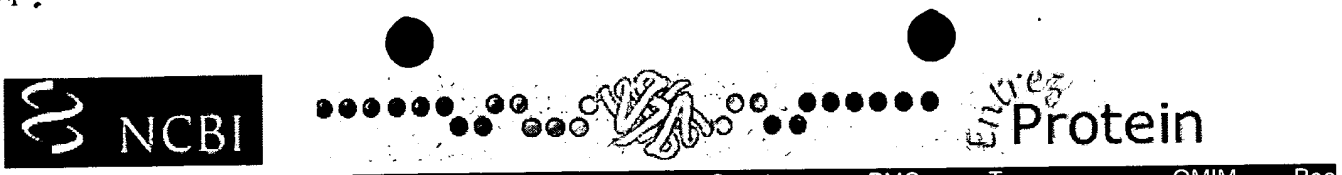
BLink, Domains, Links

```
LOCUS       BAB17787                1851 aa            linear   ROD 11-NOV-2000
DEFINITION  mucin [Rattus norvegicus].
ACCESSION   BAB17787
VERSION     BAB17787.1  GI:11138240
DBSOURCE    accession AB042530.1
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (sites)
  AUTHORS   Oinuma,T. and Suganuma,T.
  TITLE     Rat gastric mucin Muc5AC: Sequence of its 5'-region contains
            conserved D-domains and two leucine zipper motifs
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 1851)
  AUTHORS   Oinuma,T., Oinuma,T. and Suganuma,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2000) Tsutomu Oinuma, Miyazaki Medical College,
            Department of Anatomy; Kihara 5200, Kiyotake, Miyazaki 8891692,
            Japan (E-mail:tu@gray.miyazaki-med.ac.jp, Tel:81985851784,
            Fax:81985858406)
FEATURES             Location/Qualifiers
     source          1..1851
                     /organism="Rattus norvegicus"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /sex="male"
                     /tissue_type="stomach"
     Protein         1..1851
                     /product="mucin"
     CDS             1..1851
                     /gene="Muc5AC"
                     /coded_by="AB042530.1:28..>5580"

ORIGIN
        1 mlhsmgvgrr klapfwvlal altfnqhtgq aledtrkshl ehysdlsqpq ghvgtplnrv
       61 tiipplktip vvrafnpaht rrvcstwgnf hyktfdgqvf yfpglcnyvf sehcgaayed
      121 fniqlrrgle snsttlsrvi mkldglvvel tkssvlvnnh pvqlpfsqsg vlielsngyl
      181 kvvarlglvf mwnddds111 eldtkyankt cglcgdfngs pesseflshn vrltplefgn
      241 fqkmdgpteq cqdplpvpqk ncsirssice eilkgqlfsn caalvdissy leacqqdlcl
      301 cessdpsnci chtlaeysrq cahaggqpqn wrgpnlcpqt cllnmeyqec gspcvdtcsn
      361 pqhsqvcedh cvagcfcpeg mvlddsnqtg cvpvsqcacl yngtlyapgt systdctkct
      421 csggqwscqe vpcsgtcsvm ggshistfde rqytvhgdcs yvlckpydsn aftvlaelrk
      481 cgltesetcl ktvtlnlggg ktvitvkatg evfvnqiytq lpvstanatf frpstffiig
      541 qtnlglqlei qlhpimqvsv riapefrglt sglcgnfnsm qaddfqtisg vvegtaaaff
      601 ntfktqaacp nvknifedpc slsvenekya qhwcsqltda ngpfsqchat vnpstffsnc
      661 mfdtcnceks edclcaalss yvracaakgv llsdwregic akptitcpks mtyqyhistc
      721 qptcrslsee dvtchvnfip vdgctcpkgt flddsgkcvq atscpcyykg spvpngesvh
      781 dngaictctq galtciggpv ltpvcdapmi yfdcrnatpg dtgagcqksc htldmtcyss
      841 ecvpgcvcpn glvadgngsc vvaedcpcvh neatyrpget iqvgcnnctc enrmwqctdk
```

```
 901 pclatcavyg dghyitfdgq rysfsgdcey tllqdncggn gssqdafrvv tenipcgttg
 961 ttcskgikif lgsyelklsd skmevvqkgv gqeppyfvhq mgnylvvetd iglvllwdkk
1021 tsiflrlspe fkgkvcglcg nfddnaindf ttrsqsvvsd mlefgnswkl spscpdasvs
1081 kdpctanpyr kswaqkqcsi insaafsach ahvepakyye acvndacacd sggdcecfct
1141 avaayaqach evgvcvswrt pdicplfcdy ynpegqcewh yqpcgapcmr tcqnptgqcl
1201 qdlrglegcy pkcpptapif degtmqcvsn ctvspspcrv ngklyrpgtp ipsdencysc
1261 vctesgvnct hdagacvcty ngqryhpgdt iyhttdgmgg cisahcrdng tierivdtcs
1321 stsppppttf sfsttlvmts mqpssthssp tpsvvypgsp skavltassv ssvktpetts
1381 vlttstsast ltmpacqeec lwspwmdisr pgrgidsgdf dtlenlhahg yqicpvpkav
1441 ecraednpgv pfhalqqhve csttvglicy nsdqvsglcd nyqikiqcct pincptstgp
1501 tqtthlivsr tstmedttss vpvtstehty stvasspsth tpgpspsssv psssaparst
1561 ptpvssttvk ttlpttspmp eptsatssvs istlgstlas peithgcrke lcnwtdwidg
1621 sypepgrssg dfdtfvnlra kgykfcekpw nvecraqffp ntplqelgqd vtcsrevgli
1681 clnknqlppi cynyeiriec ctivnicstt sattqptshg vsiktktnwi tntysfsten
1741 tsghstvint ktwvtgstht tpqpgtrptp sivstqdtst ssvqtdstts sshtsspntg
1801 rvstthttht sspptggtsp tstthtsspn tggtsptstt htsspxtggt s
//
```


Jul 30 2003 12:44:50



1: AAB81126. unknown [Shewanel...[gi:2529421]

BLink, Domains, Links

```
LOCUS       AAB81126                543 aa            linear   BCT 15-OCT-1997
DEFINITION  unknown [Shewanella sp. SCRC-2738].
ACCESSION   AAB81126
VERSION     AAB81126.1  GI:2529421
DBSOURCE    locus SSU73935 accession U73935.1
KEYWORDS    .
SOURCE      Shewanella sp. SCRC-2738
  ORGANISM  Shewanella sp. SCRC-2738
            Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
            Alteromonadaceae; Shewanella.
REFERENCE   1  (residues 1 to 543)
  AUTHORS   Takeyama,H., Takeda,D., Yazawa,K., Yamada,A. and Matsunaga,T.
  TITLE     Expression of the eicosapentaenoic acid synthesis gene cluster from
            Shewanella sp. in a transgenic marine cyanobacterium, Synechococcus
            sp
  JOURNAL   Microbiology 143 (Pt 8), 2725-2731 (1997)
  MEDLINE   97419510
   PUBMED   9274025
REFERENCE   2  (residues 1 to 543)
  AUTHORS   Yamada,A., Watanabe,K., Yazawa,K., Kato,S. and Kondo,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-1996) Sagami Chemical Research Centerrch arch,
            4-4-1 Nishi-Ohnuma, Sagamihara, Kanagawa 229, Japan
FEATURES             Location/Qualifiers
     source          1..543
                     /organism="Shewanella sp. SCRC-2738"
                     /strain="SCRC-2738"
                     /db_xref="taxon:53560"
                     /note="eicosapentaenoic acid (EPA) synthesis gene cluster"
     Protein         1..543
                     /product="unknown"
     CDS             1..543
                     /coded_by="U73935.1:30730..32361"
                     /note="ORF8"
                     /transl_table=11
ORIGIN
        1 mnptatneml spwpwavtes nisfdvqvme qqlkdfsrac yvvnhadhgf giaqtadivt
       61 eqaanstdlp vsaftpalgt eslgdnnfrr vhgvkyayya gamangisse elvialgqag
      121 ilcgsfgaag lipsrveaai nriqaalpng pymfnlihsp sepalergsv elflkhkvrt
      181 veasaflglt pqivyyraag lsrdaqgkvv vgnkviakvs rtevaekfmm papakmlqkl
      241 vddgsitaeq melaqlvpma dditaeadsg ghtdnrplvt llptilalke eiqakyqydt
      301 pirvgcgggv gtpdaalatf nmgaayivtg sinqacveag asdhtrklla ttemadvtma
      361 paadmfemgv klqvvkrgtl fpmranklye iytrydsiea iplderekle kqvfrsslde
      421 iwagtvahfn erdpkqiera egnpkrkmal ifrwylglss rwsnsgevgr emdyqiwagp
      481 algafnqwak gsyldnyqdr navdlakhlm ygaaylnrin sltaqgvkvp aqllrwkpnq
      541 rma
//
```